

OIEP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/878,454

DATE: 06/27/2001

TIME: 18:54:42

Input Set : A:\Calmyrin.ST25.txt

Output Set: N:\CRF3\06272001\I878454.raw

3 <110> APPLICANT: Monteiro, et al.  
 5 <120> TITLE OF INVENTION: Method of Controlling the Binding of Calmyrin to Presenilin  
 7 <130> FILE REFERENCE: 4115-161  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/878,454  
 C--> 9 <141> CURRENT FILING DATE: 2001-06-11  
 9 <150> PRIOR APPLICATION NUMBER: 60/210,939  
 10 <151> PRIOR FILING DATE: 2000-06-11  
 12 <160> NUMBER OF SEQ ID NOS: 26  
 14 <170> SOFTWARE: PatentIn version 3.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 448  
 18 <212> TYPE: PRT  
 19 <213> ORGANISM: Homo sapiens  
 21 <400> SEQUENCE: 1  
 23 Met Leu Thr Phe Met Ala Ser Asp Ser Glu Glu Glu Val Cys Asp Glu  
 24 1 5 10 15  
 27 Arg Thr Ser Leu Met Ser Ala Glu Ser Pro Thr Pro Arg Ser Cys Gln  
 28 20 25 30  
 31 Glu Gly Arg Gln Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg  
 32 35 40 45  
 35 Ser Gln Glu Asn Glu Glu Asp Gly Glu Glu Asp Pro Asp Arg Tyr Val  
 36 50 55 60  
 39 Cys Ser Gly Val Pro Gly Arg Pro Pro Gly Leu Glu Glu Glu Leu Thr  
 40 65 70 75 80  
 43 Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr  
 44 85 90 95  
 47 Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr  
 48 100 105 110  
 51 Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr  
 52 115 120 125  
 55 Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile  
 56 130 135 140  
 59 Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr  
 60 145 150 155 160  
 63 Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser  
 64 165 170 175  
 67 Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Leu  
 68 180 185 190  
 71 Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Leu Leu Thr Val  
 72 195 200 205  
 75 Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro  
 76 210 215 220  
 79 Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala  
 80 225 230 235 240  
 83 Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu  
 84 245 250 255  
 87 Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly

ENTERED

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88          260          265          270
91 Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile
92          275          280          285
95 Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met
96          290          295          300
99 Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp
100 305          310          315          320
103 Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr
104          325          330          335
107 Pro Glu Val Phe Glu Pro Pro Leu Thr Gly Tyr Pro Gly Glu Glu Leu
108          340          345          350
111 Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile
112          355          360          365
115 Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Ser Gly Asp
116          370          375          380
119 Trp Asn Thr Thr Leu Ala Cys Phe Val Ala Ile Leu Ile Gly Leu Cys
120 385          390          395          400
123 Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu
124          405          410          415
127 Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn
128          420          425          430
131 Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His Gln Leu Tyr Ile
132          435          440          445
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 191
137 <212> TYPE: PRT
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 2
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143 1          5          10          15
146 Gln Asp Leu Thr Phe Leu Thr Lys Gln Glu Ile Leu Leu Ala His Arg
147          20          25          30
150 Arg Phe Cys Glu Leu Leu Pro Gln Glu Gln Arg Thr Val Glu Ser Ser
151          35          40          45
154 Leu Arg Ala Gln Val Pro Phe Glu Gln Ile Leu Ser Leu Pro Glu Leu
155          50          55          60
158 Lys Ala Asn Pro Phe Lys Glu Arg Ile Cys Arg Val Phe Ser Thr Ser
159 65          70          75          80
162 Pro Ala Lys Asp Ser Leu Ser Phe Glu Asp Phe Leu Asp Leu Leu Ser
163          85          90          95
166 Val Phe Ser Asp Thr Ala Thr Pro Asp Ile Lys Ser His Tyr Ala Phe
167          100         105         110
170 Arg Ile Phe Asp Phe Asp Asp Asp Gly Thr Leu Asn Arg Glu Asp Leu
171          115         120         125
174 Ser Arg Leu Val Asn Cys Leu Thr Gly Glu Gly Glu Asp Thr Arg Leu
175          130         135         140
178 Ser Ala Ser Glu Met Lys Gln Leu Ile Asp Asn Ile Leu Glu Glu Ser
179 145         150         155         160
182 Asp Ile Asp Arg Asp Gly Thr Ile Asn Leu Ser Glu Phe Gln His Val

```

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```

183           165           170           175
186 Ile Ser Arg Ser Pro Asp Phe Ala Ser Ser Phe Lys Ile Val Leu
187           180           185           190
190 <210> SEQ ID NO: 3
191 <211> LENGTH: 467
192 <212> TYPE: PRT
193 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 3
197 Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
198 1           5           10           15
201 Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
202           20           25           30
205 Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
206           35           40           45
209 Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
210           50           55           60
213 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
214 65           70           75           80
217 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
218           85           90           95
221 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
222           100          105          110
225 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
226           115          120          125
229 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
230           130          135          140
233 Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
234 145          150          155          160
237 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
238           165          170          175
241 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
242           180          185          190
245 Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
246           195          200          205
249 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
250           210          215          220
253 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
254 225          230          235          240
257 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
258           245          250          255
261 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
262           260          265          270
265 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
266           275          280          285
269 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
270           290          295          300
273 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
274 305          310          315          320
277 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe

```

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```

278          325          330          335
281 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
282          340          345          350
285 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
286          355          360          365
289 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
290          370          375          380
293 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
294 385          390          395          400
297 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
298          405          410          415
301 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
302          420          425          430
305 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
306          435          440          445
309 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
310          450          455          460
313 Phe Tyr Ile
314 465

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317 &lt;210&gt; SEQ ID NO: 4

318 &lt;211&gt; LENGTH: 34

319 &lt;212&gt; TYPE: DNA

320 &lt;213&gt; ORGANISM: Homo sapiens

322 &lt;400&gt; SEQUENCE: 4

323 gctgagtacg ctcgaggtag gggagctgga gggc

34

326 &lt;210&gt; SEQ ID NO: 5

327 &lt;211&gt; LENGTH: 31

328 &lt;212&gt; TYPE: DNA

329 &lt;213&gt; ORGANISM: Homo sapiens

331 &lt;400&gt; SEQUENCE: 5

332 cgcttctgga attccccaaa gggcctctga g

31

335 &lt;210&gt; SEQ ID NO: 6

336 &lt;211&gt; LENGTH: 33

337 &lt;212&gt; TYPE: DNA

338 &lt;213&gt; ORGANISM: Homo sapiens

340 &lt;400&gt; SEQUENCE: 6

341 gctagcatcg ctcgagccac accatggcag atg

33

344 &lt;210&gt; SEQ ID NO: 7

345 &lt;211&gt; LENGTH: 29

346 &lt;212&gt; TYPE: DNA

347 &lt;213&gt; ORGANISM: Homo sapiens

349 &lt;400&gt; SEQUENCE: 7

350 cgcttctgga attccccacg gttggcatg

29

353 &lt;210&gt; SEQ ID NO: 8

354 &lt;211&gt; LENGTH: 33

355 &lt;212&gt; TYPE: DNA

356 &lt;213&gt; ORGANISM: Homo sapiens

358 &lt;400&gt; SEQUENCE: 8

359 tatcgcttaa gtcgacgatg tagagctgat ggg

33

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Input Set : A:\Calmyrin.ST25.txt

Output Set: N:\CRF3\06272001\I878454.raw

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362 <210> SEQ ID NO: 9
363 <211> LENGTH: 28
364 <212> TYPE: DNA
365 <213> ORGANISM: Homo sapiens
367 <400> SEQUENCE: 9
368 cggtacgtga attcaagaag gcgctgcc                28
371 <210> SEQ ID NO: 10
372 <211> LENGTH: 33
373 <212> TYPE: DNA
374 <213> ORGANISM: Homo sapiens
376 <400> SEQUENCE: 10
377 gctagcatcg ctcgagatac ttggaatttt tgg          33
380 <210> SEQ ID NO: 11
381 <211> LENGTH: 33
382 <212> TYPE: DNA
383 <213> ORGANISM: Homo sapiens
385 <400> SEQUENCE: 11
386 cgtcatcagc gaattcccga aaggtccact tcg          33
389 <210> SEQ ID NO: 12
390 <211> LENGTH: 33
391 <212> TYPE: DNA
392 <213> ORGANISM: Homo sapiens
394 <400> SEQUENCE: 12
395 ctcgcctagc ctcgagccac accattgttg agg          33
398 <210> SEQ ID NO: 13
399 <211> LENGTH: 37
400 <212> TYPE: DNA
401 <213> ORGANISM: Homo sapiens
403 <400> SEQUENCE: 13
404 tcgtgaggat cctcgagcta ctggagccgc gacaggc      37
407 <210> SEQ ID NO: 14
408 <211> LENGTH: 34
409 <212> TYPE: DNA
410 <213> ORGANISM: Homo sapiens
412 <400> SEQUENCE: 14
413 ctagacctga attcccaatg gcgactgcga cccc        34
416 <210> SEQ ID NO: 15
417 <211> LENGTH: 34
418 <212> TYPE: DNA
419 <213> ORGANISM: Homo sapiens
421 <400> SEQUENCE: 15
422 cgagtagcat gtcgaccagg acaatcttaa agga        34
425 <210> SEQ ID NO: 16
426 <211> LENGTH: 33
427 <212> TYPE: DNA
428 <213> ORGANISM: Homo sapiens
430 <400> SEQUENCE: 16
431 gctacactag ccgcgggaat tcggcacgag gcg          33
434 <210> SEQ ID NO: 17

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 Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

## VERIFICATION SUMMARY

DATE: 06/27/2001

PATENT APPLICATION: US/09/878,454

TIME: 18:54:43

Input Set : A:\Calmyrin.ST25.txt

Output Set: N:\CRF3\06272001\I878454.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25

L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25

L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25